

Arun Durvasula

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7483027/publications.pdf>

Version: 2024-02-01

12
papers

1,082
citations

840776

11
h-index

1199594

12
g-index

17
all docs

17
docs citations

17
times ranked

2210
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Natural selection interacts with recombination to shape the evolution of hybrid genomes. <i>Science</i> , 2018, 360, 656-660. | 12.6 | 314 |
| 2 | African genomes illuminate the early history and transition to selfing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5213-5218. | 7.1 | 142 |
| 3 | A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, . | 6.0 | 112 |
| 4 | Recent demography drives changes in linked selection across the maize genome. <i>Nature Plants</i> , 2016, 2, 16084. | 9.3 | 111 |
| 5 | Recovering signals of ghost archaic introgression in African populations. <i>Science Advances</i> , 2020, 6, eaax5097. | 10.3 | 100 |
| 6 | Gene expression drives the evolution of dominance. <i>Nature Communications</i> , 2018, 9, 2750. | 12.8 | 97 |
| 7 | Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. <i>Molecular Biology and Evolution</i> , 2018, 35, 1190-1209. | 8.9 | 45 |
| 8 | A statistical model for reference-free inference of archaic local ancestry. <i>PLoS Genetics</i> , 2019, 15, e1008175. | 3.5 | 31 |
| 9 | Negative selection on complex traits limits phenotype prediction accuracy between populations. <i>American Journal of Human Genetics</i> , 2021, 108, 620-631. | 6.2 | 30 |
| 10 | Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. <i>Science</i> , 2021, 371, 415-419. | 12.6 | 27 |
| 11 | Advancing admixture graph estimation via maximum likelihood network orientation. <i>Bioinformatics</i> , 2021, 37, i142-i150. | 4.1 | 21 |
| 12 | <sc>angsd</sc>â€ wrapper: utilities for analysing nextâ€ generation sequencing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1449-1454. | 4.8 | 18 |